



SEQUENCE LISTING

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PUEHLER, ALFRED
BINDER, MICHAEL
GREISSINGER, DIETER
THIERBACH, GEORG

<120> NUCLEOTIDE SEQUENCES WHICH CODE FOR THE METY GENE

<130> 211707USOX

<140> 09/919,932

<141> 2001-08-02

<150> DE 10043334.0

<151> 2000-09-02

<150> DE 10109690.9

<151> 2001-02-28

<150> US 60/294,252

<151> 2001-05-31

<160> 6

<170> PatentIn version 3.2

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<212> DNA

<213> Corynebacterium glutamicum

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gtctattgca atagaccaag ctgttcagta ggggtgcatgg gagaagaatt tcctaataaa 180
aactcttaag gacctccaa atg cca aag tac gac aat tcc aat gct gac cag 232
Met Pro Lys Tyr Asp Asn Ser Asn Ala Asp Gln 10
1
tgg ggc ttt gaa acc cgc tcc att cac gca ggc cag tca gta gac gca 280
Trp Gly Phe Glu Thr Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala 25
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cag acc agc gca cga aac ctt ccg atc tac caa tcc acc gct ttc gtg 328
Gln Thr Ser Ala Arg Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val 40
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ttc gac tcc gct gag cac gcc aag cag cgt ttc gca ctt gag gat cta 376
Phe Asp Ser Ala Glu His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu 55
45
ggc cct gtt tac tcc cgc ctc acc aac cca acc gtt gag gct ttg gaa 424
Gly Pro Val Tyr Ser Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu 75
60 65 70 75

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| aac cgc atc gct tcc ctc gaa ggt ggc gtc cac gct gta gcg ttc tcc Asn Arg Ile Ala Ser Leu Glu Gly Gly Val His Ala Val Ala Phe Ser 80 85 90 | 472 |
| tcc gga cag gcc gca acc acc aac gcc att ttg aac ctg gca gga gcg Ser Gly Gln Ala Ala Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala 95 100 105 | 520 |
| ggc gac cac atc gtc acc tcc cca cgc ctc tac ggt ggc acc gag act Gly Asp His Ile Val Thr Ser Pro Arg Leu Tyr Gly Thr Glu Thr 110 115 120 | 568 |
| cta ttc ctt atc act ctt aac cgc ctg ggt atc gat gtt tcc ttc gtg Leu Phe Leu Ile Thr Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val 125 130 135 | 616 |
| gaa aac ccc gac gac cct gag tcc tgg cag gca gcc gtt cag cca aac Glu Asn Pro Asp Asp Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn 140 145 150 155 | 664 |
| acc aaa gca ttc ttc ggc gag act ttc gcc aac cca cag gca gac gtc Thr Lys Ala Phe Phe Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val 160 165 170 | 712 |
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| ggc aac ggc tcc gga ctg ggc ggc gtg ctt atc gac ggc gga aag ttc Gly Asn Gly Ser Gly Leu Gly Gly Val Leu Ile Asp Gly Gly Lys Phe 220 225 230 235 | 904 |
| gat tgg act gtc gaa aag gat gga aag cca gta ttc ccc tac ttc gtc Asp Trp Thr Val Glu Lys Asp Gly Lys Pro Val Phe Pro Tyr Phe Val 240 245 250 | 952 |
| act cca gat gct gct tac cac gga ttg aag tac gca gac ctt ggt gca Thr Pro Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala 255 260 265 | 1000 |
| cca gcc ttc ggc ctc aag gtt cgc gtt ggc ctt cta cgc gac acc ggc Pro Ala Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly 270 275 280 | 1048 |
| tcc acc ctc tcc gca ttc aac gca tgg gct gca gtc cag ggc atc gac Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp 285 290 295 | 1096 |
| acc ctt tcc ctg cgc ctg gag cgc cac aac gaa aac gcc atc aag gtt Thr Leu Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val 300 305 310 315 | 1144 |
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| ggc ctg aag gat tcc cct tgg tac gca acc aag gaa aag ctt ggc ctg Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu 335 340 345 | 1240 |
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 gag gct tgg gca ttt atc gac gcc ctg aag cta cac tcc aac ctt gca 1336
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 aac atc ggc gat gtt cgc tcc ctg gtt gtt cac cca gca acc acc acc 1384
 Asn Ile Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr
 380 385 390 395
 cat tca cag tcc gac gaa gct ggc ctg gca cgc gcg ggc gtt acc cag 1432
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 400 405 410
 tcc acc gtc cgc ctg tcc gtt ggc atc gag acc att gat gat atc atc 1480
 Ser Thr Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile
 415 420 425
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 Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile 435
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 acagagctgt ccatatacac tggacgaagt tttagtcttg tccaccacaga acaggcgggt 1650
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 35 40 45
 His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser
 50 55 60
 Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser
 65 70 75 80
 Leu Glu Gly Gly Val His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala
 85 90 95
 Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val
 100 105 110
 Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr
 115 120 125

Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp
130 135 140

Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe
145 150 155 160

Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val Leu Asp Ile Pro Ala
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Val Ala Glu Val Ala His Arg Asn Ser Val Pro Leu Ile Ile Asp Asn
180 185 190

Thr Ile Ala Thr Ala Ala Leu Val Arg Pro Leu Glu Leu Gly Ala Asp
195 200 205

Val Val Val Ala Ser Leu Thr Lys Phe Tyr Thr Gly Asn Gly Ser Gly
210 215 220

Leu Gly Gly Val Leu Ile Asp Gly Gly Lys Phe Asp Trp Thr Val Glu
225 230 235 240

Lys Asp Gly Lys Pro Val Phe Pro Tyr Phe Val Thr Pro Asp Ala Ala
245 250 255

Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu
260 265 270

Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala
275 280 285

Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg
290 295 300

Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn
305 310 315 320

Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser
325 330 335

Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser
340 345 350

Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe
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Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val
370 375 380

Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser Gln Ser Asp
385 390 395 400

Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu
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